



SEQUENCE LISTING

<110> ULLRICH, AXEL
GISHIZKY, MIKHAIL
SURES, IRMINGARD

<120> NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES

<130> 038602/1259

<140> 09/977,261

<141> 2001-10-16

<150> 08/232,545

<151> 1994-04-22

<160> 24

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Unknown Organism

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<221> CDS

<222> (258)..(1778)

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<223> Description of Unknown Organism: Megakaryocyte
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Met Ala Gly Arg Gly Ser Leu Val Ser Trp Arg
1 5 10
gca ttt cac ggc tgt gat tct gct gag gaa ctt ccc cgg gtg agc ccc 338
Ala Phe His Gly Cys Asp Ser Ala Glu Glu Leu Pro Arg Val Ser Pro
15 20 25
cgc ttc ctc cga gcc tgg cac ccc cct ccc gtc tca gcc agg atg cca 386
Arg Phe Leu Arg Ala Trp His Pro Pro Pro Val Ser Ala Arg Met Pro
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acg agg cgc tgg gcc ccg ggc acc cag tgt atc acc aaa tgc gag cac 434
Thr Arg Arg Trp Ala Pro Gly Thr Gln Cys Ile Thr Lys Cys Glu His
45 50 55

214

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Thr Arg Pro Lys Pro Gly Glu Leu Ala Phe Arg Lys Gly Asp Val Val	
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acc atc ctg gag gcc tgc gag aac aag agc tgg tac cgc gtc aag cac	530
Thr Ile Leu Glu Ala Cys Glu Asn Lys Ser Trp Tyr Arg Val Lys His	
80 85 90	
cac acc agt gga cag gag ggg ctg ctg gca gct ggg gcg ctg cgg gag	578
His Thr Ser Gly Gln Glu Gly Leu Leu Ala Ala Gly Ala Leu Arg Glu	
95 100 105	
cgg gag gcc ctc tcc gca gac ccc aag ctc agc ctc atg ccg tgg ttc	626
Arg Glu Ala Leu Ser Ala Asp Pro Lys Leu Ser Leu Met Pro Trp Phe	
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cac ggg aag atc tcg ggc cag gag gct gtc cag cag ctg cag cct ccc	674
His Gly Lys Ile Ser Gly Gln Glu Ala Val Gln Gln Leu Gln Pro Pro	
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Glu Asp Gly Leu Phe Leu Val Arg Glu Ser Ala Arg His Pro Gly Asp	
140 145 150 155	
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Tyr Val Leu Cys Val Ser Phe Gly Arg Asp Val Ile His Tyr Arg Val	
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Leu His Arg Asp Gly His Leu Thr Ile Asp Glu Ala Val Phe Phe Cys	
175 180 185	
aac ctc atg gac atg gtg gag cat tac agc aag gac aag ggc gct atc	866
Asn Leu Met Asp Met Val Glu His Tyr Ser Lys Asp Lys Gly Ala Ile	
190 195 200	
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Cys Thr Lys Leu Val Arg Pro Lys Arg Lys His Gly Thr Lys Ser Ala	
205 210 215	
gag gag gag ctg gcc agg gcg ggc tgg tta ctg aac ctg cag cat ttg	962
Glu Glu Glu Leu Ala Arg Ala Gly Trp Leu Leu Asn Leu Gln His Leu	
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aca ttg gga gca cag atc gga gag gga gag ttt gga gct gtc ctg cag	1010
Thr Leu Gly Ala Gln Ile Gly Glu Gly Glu Phe Gly Ala Val Leu Gln	
240 245 250	
ggt gag tac ctg ggg caa aag gtg gcc gtg aag aat atc aag tgt gat	1058
Gly Glu Tyr Leu Gly Gln Lys Val Ala Val Lys Asn Ile Lys Cys Asp	
255 260 265	
gtg aca gcc cag gcc ttc ctg gac gag acg gcc gtc atg acg aag atg	1106
Val Thr Ala Gln Ala Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met	
270 275 280	

Q14
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ctg tac att gtc atg gag cac gtg agc aag ggc aac ctg gtg aac ttt Leu Tyr Ile Val Met Glu His Val Ser Lys Gly Asn Leu Val Asn Phe 300 305 310 315	1202
ctg cgg acc cgg ggt cga gcc ctc gtg aac acc gct cag ctc ctg cag Leu Arg Thr Arg Gly Arg Ala Leu Val Asn Thr Ala Gln Leu Leu Gln 320 325 330	1250
ttt tct ctg cac gtg gcc gag ggc atg gag tac ctg gag agc aag aag Phe Ser Leu His Val Ala Glu Gly Met Glu Tyr Leu Glu Ser Lys Lys 335 340 345	1298
ctt gtg cac cgc gac ctg gcc gcc cgc aac atc ctg gtc tca gag gac Leu Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Ser Glu Asp 350 355 360	1346
ctg gtg gcc aag gtc agc gac ttt ggc ctg gcc aaa gcc gag cgg aag Leu Val Ala Lys Val Ser Asp Phe Gly Leu Ala Lys Ala Glu Arg Lys 365 370 375	1394
ggg cta gac tca agc cgg ctg ccc gtc aag tgg acg gcg ccc gag gct Gly Leu Asp Ser Ser Arg Leu Pro Val Lys Trp Thr Ala Pro Glu Ala 380 385 390 395	1442
ctc aaa cac ggg aag ttc acc agc aag tcg gat gtc tgg agt ttt ggg Leu Lys His Gly Lys Phe Thr Ser Lys Ser Asp Val Trp Ser Phe Gly 400 405 410	1490
gtg ctg ctc tgg gag gtc ttc tca tat gga cgg gct ccg tac cct aaa Val Leu Leu Trp Glu Val Phe Ser Tyr Gly Arg Ala Pro Tyr Pro Lys 415 420 425	1538
atg tca ctg aaa gag gtg tcg gag gcc gtg gag aag ggg tac cgc atg Met Ser Leu Lys Glu Val Ser Glu Ala Val Glu Lys Gly Tyr Arg Met 430 435 440	1586
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<223> Description of Unknown Organism: Megakaryocyte
kinase 1

<400> 2

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Trp	His	Pro	Pro	Pro	Val	Ser	Ala	Arg	Met	Pro	Thr	Arg	Arg	Trp	Ala	35	40	45	
Pro	Gly	Thr	Gln	Cys	Ile	Thr	Lys	Cys	Glu	His	Thr	Arg	Pro	Lys	Pro	50	55	60	
Gly	Glu	Leu	Ala	Phe	Arg	Lys	Gly	Asp	Val	Val	Thr	Ile	Leu	Glu	Ala	65	70	75	80
Cys	Glu	Asn	Lys	Ser	Trp	Tyr	Arg	Val	Lys	His	His	Thr	Ser	Gly	Gln	85	90	95	
Glu	Gly	Leu	Leu	Ala	Ala	Gly	Ala	Leu	Arg	Glu	Arg	Glu	Ala	Leu	Ser	100	105	110	
Ala	Asp	Pro	Lys	Leu	Ser	Leu	Met	Pro	Trp	Phe	His	Gly	Lys	Ile	Ser	115	120	125	
Gly	Gln	Glu	Ala	Val	Gln	Gln	Leu	Gln	Pro	Pro	Glu	Asp	Gly	Leu	Phe	130	135	140	
Leu	Val	Arg	Glu	Ser	Ala	Arg	His	Pro	Gly	Asp	Tyr	Val	Leu	Cys	Val	145	150	155	160
Ser	Phe	Gly	Arg	Asp	Val	Ile	His	Tyr	Arg	Val	Leu	His	Arg	Asp	Gly	165	170	175	
His	Leu	Thr	Ile	Asp	Glu	Ala	Val	Phe	Phe	Cys	Asn	Leu	Met	Asp	Met	180	185	190	
Val	Glu	His	Tyr	Ser	Lys	Asp	Lys	Gly	Ala	Ile	Cys	Thr	Lys	Leu	Val	195	200	205	
Arg	Pro	Lys	Arg	Lys	His	Gly	Thr	Lys	Ser	Ala	Glu	Glu	Glu	Leu	Ala	210	215	220	

Arg Ala Gly Trp Leu Leu Asn Leu Gln His Leu Thr Leu Gly Ala Gln
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 Ile Gly Glu Gly Glu Phe Gly Ala Val Leu Gln Gly Glu Tyr Leu Gly
 245 250 255
 Gln Lys Val Ala Val Lys Asn Ile Lys Cys Asp Val Thr Ala Gln Ala
 260 265 270
 Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met Gln His Glu Asn Leu
 275 280 285
 Val Arg Leu Leu Gly Val Ile Leu His Gln Gly Leu Tyr Ile Val Met
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 Glu His Val Ser Lys Gly Asn Leu Val Asn Phe Leu Arg Thr Arg Gly
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 Arg Ala Leu Val Asn Thr Ala Gln Leu Leu Gln Phe Ser Leu His Val
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 Ala Glu Gly Met Glu Tyr Leu Glu Ser Lys Lys Leu Val His Arg Asp
 340 345 350
 Leu Ala Ala Arg Asn Ile Leu Val Ser Glu Asp Leu Val Ala Lys Val
 355 360 365
 Ser Asp Phe Gly Leu Ala Lys Ala Glu Arg Lys Gly Leu Asp Ser Ser
 370 375 380
 Arg Leu Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Lys His Gly Lys
 385 390 395 400
 Phe Thr Ser Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu
 405 410 415
 Val Phe Ser Tyr Gly Arg Ala Pro Tyr Pro Lys Met Ser Leu Lys Glu
 420 425 430
 Val Ser Glu Ala Val Glu Lys Gly Tyr Arg Met Glu Pro Pro Glu Gly
 435 440 445
 Cys Pro Gly Pro Val His Val Leu Met Ser Ser Cys Trp Glu Ala Glu
 450 455 460
 Pro Ala Arg Arg Pro Pro Phe Arg Lys Leu Ala Glu Lys Leu Ala Arg
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<222> (82)..(2106)

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<223> Description of Unknown Organism: Megakaryocyte
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                        Met Asp Thr Lys Ser Ile Leu Glu Glu Leu
                        1                      5                      10

ctt ctc aaa aga tca cag caa aag aag aaa atg tca cca aat aat tac 159
Leu Leu Lys Arg Ser Gln Gln Lys Lys Lys Met Ser Pro Asn Asn Tyr
                        15                      20                      25

aaa gaa cgg ctt ttt gtt ttg acc aaa aca aac ctt tcc tac tat gaa 207
Lys Glu Arg Leu Phe Val Leu Thr Lys Thr Asn Leu Ser Tyr Tyr Glu
                        30                      35                      40

tat gac aaa atg aaa agg ggc agc aga aaa gga tcc att gaa att aag 255
Tyr Asp Lys Met Lys Arg Gly Ser Arg Lys Gly Ser Ile Glu Ile Lys
                        45                      50                      55

aaa atc aga tgt gtg gag aaa gta aat ctc gag gag cag acg cct gta 303
Lys Ile Arg Cys Val Glu Lys Val Asn Leu Glu Glu Gln Thr Pro Val
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gag aga cag tac cca ttt cag att gtc tat aaa gat ggg ctt ctc tat 351
Glu Arg Gln Tyr Pro Phe Gln Ile Val Tyr Lys Asp Gly Leu Leu Tyr
                        75                      80                      85                      90

gtc tat gca tca aat gaa gag agc cga agt cag tgg ttg aaa gca tta 399
Val Tyr Ala Ser Asn Glu Glu Ser Arg Ser Gln Trp Leu Lys Ala Leu
                        95                      100                      105

caa aaa gag ata agg ggt aac ccc cac ctg ctg gtc aag tac cat agt 447
Gln Lys Glu Ile Arg Gly Asn Pro His Leu Leu Val Lys Tyr His Ser
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ggg ttc ttc gtg gac ggg aag ttc ctg tgt tgc cag cag agc tgt aaa 495
Gly Phe Phe Val Asp Gly Lys Phe Leu Cys Cys Gln Gln Ser Cys Lys
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gca gcc cca gga tgt acc ctc tgg gaa gca tat gct aat ctg cat act 543
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gca gtc aat gaa gag aaa cac aga gtt ccc acc ttc cca gac aga gtg 591
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ggc tcc cag cca cca tct tca agt acc agt cta gcg caa tat gac agc	735
Gly Ser Gln Pro Pro Ser Ser Ser Thr Ser Leu Ala Gln Tyr Asp Ser	
205 210 215	
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Asn Ser Lys Lys Ile Tyr Gly Ser Gln Pro Asn Phe Asn Met Gln Tyr	
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Ile Pro Arg Glu Asp Phe Pro Asp Trp Trp Gln Val Arg Lys Leu Lys	
235 240 245 250	
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aat gtg aat cac acc acc tca aag att tca tgg gaa ttc cct gag tca	927
Asn Val Asn His Thr Thr Ser Lys Ile Ser Trp Glu Phe Pro Glu Ser	
270 275 280	
agt tca tct gaa gaa gag gaa aac ctg gat gat tat gac tgg ttt gct	975
Ser Ser Ser Glu Glu Glu Glu Asn Leu Asp Asp Tyr Asp Trp Phe Ala	
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Gly Asn Ile Ser Arg Ser Gln Ser Glu Gln Leu Leu Arg Gln Lys Gly	
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Lys Glu Gly Ala Phe Met Val Arg Asn Ser Ser Gln Val Gly Met Tyr	
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Lys His Tyr His Val His Thr Asn Ala Glu Asn Lys Leu Tyr Leu Ala	
350 355 360	
gaa aac tac tgt ttt gat tcc att cca aag ctt att cat tat cat caa	1215
Glu Asn Tyr Cys Phe Asp Ser Ile Pro Lys Leu Ile His Tyr His Gln	
365 370 375	
cac aat tca gca ggc atg atc aca cgg ctc cgc cac cct gtg tca aca	1263
His Asn Ser Ala Gly Met Ile Thr Arg Leu Arg His Pro Val Ser Thr	
380 385 390	

aag gcc aac aag gtc ccc gac tct gtg tcc ctg gga aat gga atc tgg	1311
Lys Ala Asn Lys Val Pro Asp Ser Val Ser Leu Gly Asn Gly Ile Trp	
395 400 405 410	
 gaa ctg aaa aga gaa gag att acc ttg ttg aag gag ctg gga agt ggc	1359
Glu Leu Lys Arg Glu Glu Ile Thr Leu Leu Lys Glu Leu Gly Ser Gly	
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Gln Phe Gly Val Val Gln Leu Gly Lys Trp Lys Gly Gln Tyr Asp Val	
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Ala Val Lys Met Ile Lys Glu Gly Ser Met Ser Glu Asp Glu Phe Phe	
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475 480 485 490	
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Tyr Ile Ser Asn Gly Cys Leu Leu Asn Tyr Leu Arg Ser His Gly Lys	
495 500 505	
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Phe Gly Met Thr Arg Tyr Val Leu Asp Asp Gln Tyr Val Ser Ser Val	
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Gly Thr Lys Phe Pro Val Lys Trp Ser Ala Pro Glu Val Phe His Tyr	
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Phe Lys Tyr Ser Ser Lys Ser Asp Val Trp Ala Phe Gly Ile Leu Met	
590 595 600	
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Trp Glu Val Phe Ser Leu Gly Lys Gln Pro Tyr Asp Leu Tyr Asp Asn	
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Ser Gln Val Val Leu Lys Val Ser Gln Gly His Arg Leu Tyr Arg Pro
620 625 630

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655 660 665

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Glu Pro Leu Arg Glu Lys Asp Lys His
670 675

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<223> Description of Unknown Organism: Megakaryocyte kinase 2

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Gly Ser Arg Lys Gly Ser Ile Glu Ile Lys Lys Ile Arg Cys Val Glu
50 55 60

Lys Val Asn Leu Glu Glu Gln Thr Pro Val Glu Arg Gln Tyr Pro Phe
65 70 75 80

Gln Ile Val Tyr Lys Asp Gly Leu Leu Tyr Val Tyr Ala Ser Asn Glu
85 90 95

Glu Ser Arg Ser Gln Trp Leu Lys Ala Leu Gln Lys Glu Ile Arg Gly
 100 105 110
 Asn Pro His Leu Leu Val Lys Tyr His Ser Gly Phe Phe Val Asp Gly
 115 120 125
 Lys Phe Leu Cys Cys Gln Gln Ser Cys Lys Ala Ala Pro Gly Cys Thr
 130 135 140
 Leu Trp Glu Ala Tyr Ala Asn Leu His Thr Ala Val Asn Glu Glu Lys
 145 150 155 160
 His Arg Val Pro Thr Phe Pro Asp Arg Val Leu Lys Ile Pro Arg Ala
 165 170 175
 Val Pro Val Leu Lys Met Asp Ala Pro Ser Ser Ser Thr Thr Leu Ala
 180 185 190
 Gln Tyr Asp Asn Glu Ser Lys Lys Asn Tyr Gly Ser Gln Pro Pro Ser
 195 200 205
 Ser Ser Thr Ser Leu Ala Gln Tyr Asp Ser Asn Ser Lys Lys Ile Tyr
 210 215 220
 Gly Ser Gln Pro Asn Phe Asn Met Gln Tyr Ile Pro Arg Glu Asp Phe
 225 230 235 240
 Pro Asp Trp Trp Gln Val Arg Lys Leu Lys Ser Ser Ser Ser Ser Glu
 245 250 255
 Asp Val Ala Ser Ser Asn Gln Lys Glu Arg Asn Val Asn His Thr Thr
 260 265 270
 Ser Lys Ile Ser Trp Glu Phe Pro Glu Ser Ser Ser Ser Glu Glu Glu
 275 280 285
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 Glu Gly Ser Met Ser Glu Asp Glu Phe Phe Gln Glu Ala Gln Thr Met
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 Met Lys Leu Ser His Pro Lys Leu Val Lys Phe Tyr Gly Val Cys Ser
 465 470 475 480
 Lys Glu Tyr Pro Ile Tyr Ile Val Thr Glu Tyr Ile Ser Asn Gly Cys
 485 490 495
 Leu Leu Asn Tyr Leu Arg Ser His Gly Lys Gly Leu Glu Pro Ser Gln
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 Leu Leu Glu Met Cys Tyr Asp Val Cys Glu Gly Met Ala Phe Leu Glu
 515 520 525
 Ser His Gln Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Leu Val
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 Val Leu Asp Asp Gln Tyr Val Ser Ser Val Gly Thr Lys Phe Pro Val
 565 570 575
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 Ser Asp Val Trp Ala Phe Gly Ile Leu Met Trp Glu Val Phe Ser Leu
 595 600 605
 Gly Lys Gln Pro Tyr Asp Leu Tyr Asp Asn Ser Gln Val Val Leu Lys
 610 615 620
 Val Ser Gln Gly His Arg Leu Tyr Arg Pro His Leu Ala Ser Asp Thr
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 Ile Tyr Gln Ile Met Tyr Ser Cys Trp His Glu Leu Pro Glu Lys Arg
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 <222> (366)..(1880)

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 kinase 3

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 gcaca atg agc aac atc tgt cag agg ctc tgg gag tac cta gaa ccc tat 410
 Met Ser Asn Ile Cys Gln Arg Leu Trp Glu Tyr Leu Glu Pro Tyr
 1 5 10 15
 ctc ccc tgt ttg tcc acg gag gca gac aag tca acc gtg att gaa aat 458
 Leu Pro Cys Leu Ser Thr Glu Ala Asp Lys Ser Thr Val Ile Glu Asn
 20 25 30
 cca ggg gcc ctt tgc tct ccc cag tca cag agg cat ggc cac tac ttt 506
 Pro Gly Ala Leu Cys Ser Pro Gln Ser Gln Arg His Gly His Tyr Phe
 35 40 45
 gtg gct ttg ttt gat tac cag gct cgg act gct gag gac ttg agc ttc 554
 Val Ala Leu Phe Asp Tyr Gln Ala Arg Thr Ala Glu Asp Leu Ser Phe
 50 55 60
 cga gca ggt gac aaa ctt caa gtt ctg gac act ttg cat gag ggc tgg 602
 Arg Ala Gly Asp Lys Leu Gln Val Leu Asp Thr Leu His Glu Gly Trp
 65 70 75
 tgg ttt gcc aga cac ttg gag aaa aga cga gat ggc tcc agt cag caa 650
 Trp Phe Ala Arg His Leu Glu Lys Arg Arg Asp Gly Ser Ser Gln Gln
 80 85 90 95
 cta caa ggc tat att cct tct aac tac gtg gct gag gac aga agc cta 698
 Leu Gln Gly Tyr Ile Pro Ser Asn Tyr Val Ala Glu Asp Arg Ser Leu
 100 105 110
 cag gca gag ccg tgg ttc ttt gga gca atc gga aga tca gat gca gag 746
 Gln Ala Glu Pro Trp Phe Phe Gly Ala Ile Gly Arg Ser Asp Ala Glu
 115 120 125

aaa	caa	cta	tta	tat	tca	gaa	aac	aag	acc	ggg	tcc	ttt	cta	atc	aga	794
Lys	Gln	Leu	Leu	Tyr	Ser	Glu	Asn	Lys	Thr	Gly	Ser	Phe	Leu	Ile	Arg	
	130						135					140				
gaa	agt	gaa	agc	caa	aaa	gga	gaa	ttc	tct	ctt	tca	gtt	tta	gat	gga	842
Glu	Ser	Glu	Ser	Gln	Lys	Gly	Glu	Phe	Ser	Leu	Ser	Val	Leu	Asp	Gly	
	145					150					155					
gca	gtt	gta	aaa	cac	tac	aga	att	aaa	aga	ctg	gat	gaa	ggg	gga	ttt	890
Ala	Val	Val	Lys	His	Tyr	Arg	Ile	Lys	Arg	Leu	Asp	Glu	Gly	Gly	Phe	
160					165					170					175	
ttt	ctc	acg	cga	aga	aga	atc	ttt	tca	aca	ctg	aac	gaa	ttt	gtg	agc	938
Phe	Leu	Thr	Arg	Arg	Arg	Ile	Phe	Ser	Thr	Leu	Asn	Glu	Phe	Val	Ser	
			180						185					190		
cac	tac	acc	aag	aca	agt	gac	ggc	ctg	tgt	gtc	aag	ctg	ggg	aaa	cca	986
His	Tyr	Thr	Lys	Thr	Ser	Asp	Gly	Leu	Cys	Val	Lys	Leu	Gly	Lys	Pro	
			195					200					205			
tgc	tta	aag	atc	cag	gtc	cca	gct	cca	ttt	gat	ttg	tcg	tat	aaa	acc	1034
Cys	Leu	Lys	Ile	Gln	Val	Pro	Ala	Pro	Phe	Asp	Leu	Ser	Tyr	Lys	Thr	
	210						215					220				
gtg	gac	caa	tgg	gag	ata	gac	cgc	aac	tcc	ata	cag	ctt	ctg	aag	cga	1082
Val	Asp	Gln	Trp	Glu	Ile	Asp	Arg	Asn	Ser	Ile	Gln	Leu	Leu	Lys	Arg	
	225					230					235					
ttg	gga	tct	ggg	cag	ttt	ggc	gaa	gta	tgg	gaa	ggg	ctg	tgg	aac	aat	1130
Leu	Gly	Ser	Gly	Gln	Phe	Gly	Glu	Val	Trp	Glu	Gly	Leu	Trp	Asn	Asn	
240				245						250					255	
acc	act	cca	gta	gca	gtg	aaa	aca	tta	aaa	cca	ggg	tca	atg	gat	cca	1178
Thr	Thr	Pro	Val	Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Ser	Met	Asp	Pro	
			260					265						270		
aat	gac	ttc	ctg	agg	gag	gca	cag	ata	atg	aag	aac	cta	aga	cat	cca	1226
Asn	Asp	Phe	Leu	Arg	Glu	Ala	Gln	Ile	Met	Lys	Asn	Leu	Arg	His	Pro	
			275					280					285			
aag	ctt	atc	cag	ctt	tat	gct	gtt	tgc	act	tta	gaa	gat	cca	att	tat	1274
Lys	Leu	Ile	Gln	Leu	Tyr	Ala	Val	Cys	Thr	Leu	Glu	Asp	Pro	Ile	Tyr	
	290						295					300				
att	att	aca	gag	ttg	atg	aga	cat	gga	agt	ctg	caa	gaa	tat	ctc	caa	1322
Ile	Ile	Thr	Glu	Leu	Met	Arg	His	Gly	Ser	Leu	Gln	Glu	Tyr	Leu	Gln	
	305					310					315					
aat	gac	act	gga	tca	aaa	atc	cat	ctg	act	caa	cag	gta	gac	atg	gcg	1370
Asn	Asp	Thr	Gly	Ser	Lys	Ile	His	Leu	Thr	Gln	Gln	Val	Asp	Met	Ala	
320					325					330					335	
gca	cag	gtt	gcc	tct	gga	atg	gcc	tat	ctg	gag	tct	cgg	aac	tac	att	1418
Ala	Gln	Val	Ala	Ser	Gly	Met	Ala	Tyr	Leu	Glu	Ser	Arg	Asn	Tyr	Ile	
			340						345					350		

cac aga gat ctg gct gcc aga aat gtc ctc gtt ggt gaa cat aat atc 1466
 His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Gly Glu His Asn Ile
 355 360 365

tac aaa gta gca gat ttt gga ctt gcc aga gtt ttt aag gta gat aat 1514
 Tyr Lys Val Ala Asp Phe Gly Leu Ala Arg Val Phe Lys Val Asp Asn
 370 375 380

gaa gac atc tat gaa tct aga cac gaa ata aag ctg ccg gtg aag tgg 1562
 Glu Asp Ile Tyr Glu Ser Arg His Glu Ile Lys Leu Pro Val Lys Trp
 385 390 395

act gcg ccc gaa gcc att cgt agt aat aaa ttc agc att aag tcc gat 1610
 Thr Ala Pro Glu Ala Ile Arg Ser Asn Lys Phe Ser Ile Lys Ser Asp
 400 405 410 415

gta tgg tca ttt gga atc ctt ctt tat gaa atc att act tat ggc aaa 1658
 Val Trp Ser Phe Gly Ile Leu Leu Tyr Glu Ile Ile Thr Tyr Gly Lys
 420 425 430

atg cct tac agt ggt atg aca ggt gcc cag gta atc cag atg ttg gct 1706
 Met Pro Tyr Ser Gly Met Thr Gly Ala Gln Val Ile Gln Met Leu Ala
 435 440 445

caa aac tat aga ctt ccg caa cca tcc aac tgt cca cag caa ttt tac 1754
 Gln Asn Tyr Arg Leu Pro Gln Pro Ser Asn Cys Pro Gln Gln Phe Tyr
 450 455 460

aac atc atg ttg gag tgc tgg aat gca gag cct aag gaa cga cct aca 1802
 Asn Ile Met Leu Glu Cys Trp Asn Ala Glu Pro Lys Glu Arg Pro Thr
 465 470 475

ttt gag aca ctg cgt tgg aaa ctt gaa gac tat ttt gaa aca gac tct 1850
 Phe Glu Thr Leu Arg Trp Lys Leu Glu Asp Tyr Phe Glu Thr Asp Ser
 480 485 490 495

tca tat tca gat gca aat aac ttc ata aga tgaacactgg agaagaatat 1900
 Ser Tyr Ser Asp Ala Asn Asn Phe Ile Arg
 500 505

caaataataa agtagcaaaa caaattcaaa taatccattc caaaatacaa tggtatcaac 1960
 caactgcaca atcagtttat cctgacatat tcaagtata ggataaagtt ggccatgtat 2020
 tatgaaaaag attatttgtg cattttattg actgggcaac actgcaggac agtcaaggctc 2080
 atatataatt gctcactgcc tggaaaatta agcacactaa accaagttat ttttcttttt 2140
 aagagatact tacatttcca tttattgttt gaaatgtcgc gatcaagaga atcaacagat 2200
 gatagtccaa tttttactca gtgatgactg tgtagcattt tctgttttac tgattagagt 2260
 ggttattcat tattcctcag attgctgaat cccatcaggc tggtattatg aaggaatttg 2320
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 ctgtaactac aatgatggta aagccatggt aaatgacttg attgtacttg gagtaattgc 2440

acattttttt ctatgcataa aaaaatgatg cagctgttga gaaaacgaag tctttttcat 2500
 tttgcagaag gaaatgatgg aatttttctg tacttcagta tgtgtcaact gagagtcata 2560
 tacattagtt ttaatctctt aatattgaga atcaggttgc aaaacggatg agttattatc 2620
 tatggaaatg tgagaaatgt ctaatagccc ataaagtctg agaaataggt atcaaaatag 2680
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<210> 6

<211> 505

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Megakaryocyte
 kinase 3

<400> 6

Met	Ser	Asn	Ile	Cys	Gln	Arg	Leu	Trp	Glu	Tyr	Leu	Glu	Pro	Tyr	Leu	1	5	10	15
Pro	Cys	Leu	Ser	Thr	Glu	Ala	Asp	Lys	Ser	Thr	Val	Ile	Glu	Asn	Pro	20	25	30	
Gly	Ala	Leu	Cys	Ser	Pro	Gln	Ser	Gln	Arg	His	Gly	His	Tyr	Phe	Val	35	40	45	
Ala	Leu	Phe	Asp	Tyr	Gln	Ala	Arg	Thr	Ala	Glu	Asp	Leu	Ser	Phe	Arg	50	55	60	
Ala	Gly	Asp	Lys	Leu	Gln	Val	Leu	Asp	Thr	Leu	His	Glu	Gly	Trp	Trp	65	70	75	80
Phe	Ala	Arg	His	Leu	Glu	Lys	Arg	Arg	Asp	Gly	Ser	Ser	Gln	Gln	Leu	85	90	95	
Gln	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Ala	Glu	Asp	Arg	Ser	Leu	Gln	100	105	110	
Ala	Glu	Pro	Trp	Phe	Phe	Gly	Ala	Ile	Gly	Arg	Ser	Asp	Ala	Glu	Lys	115	120	125	
Gln	Leu	Leu	Tyr	Ser	Glu	Asn	Lys	Thr	Gly	Ser	Phe	Leu	Ile	Arg	Glu	130	135	140	
Ser	Glu	Ser	Gln	Lys	Gly	Glu	Phe	Ser	Leu	Ser	Val	Leu	Asp	Gly	Ala	145	150	155	160
Val	Val	Lys	His	Tyr	Arg	Ile	Lys	Arg	Leu	Asp	Glu	Gly	Gly	Phe	Phe	165	170	175	
Leu	Thr	Arg	Arg	Arg	Ile	Phe	Ser	Thr	Leu	Asn	Glu	Phe	Val	Ser	His	180	185	190	

Tyr	Thr	Lys	Thr	Ser	Asp	Gly	Leu	Cys	Val	Lys	Leu	Gly	Lys	Pro	Cys		
		195					200					205					
Leu	Lys	Ile	Gln	Val	Pro	Ala	Pro	Phe	Asp	Leu	Ser	Tyr	Lys	Thr	Val		
	210					215					220						
Asp	Gln	Trp	Glu	Ile	Asp	Arg	Asn	Ser	Ile	Gln	Leu	Leu	Lys	Arg	Leu		
225					230					235					240		
Gly	Ser	Gly	Gln	Phe	Gly	Glu	Val	Trp	Glu	Gly	Leu	Trp	Asn	Asn	Thr		
				245					250					255			
Thr	Pro	Val	Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Ser	Met	Asp	Pro	Asn		
			260					265					270				
Asp	Phe	Leu	Arg	Glu	Ala	Gln	Ile	Met	Lys	Asn	Leu	Arg	His	Pro	Lys		
	275						280					285					
Leu	Ile	Gln	Leu	Tyr	Ala	Val	Cys	Thr	Leu	Glu	Asp	Pro	Ile	Tyr	Ile		
	290					295					300						
Ile	Thr	Glu	Leu	Met	Arg	His	Gly	Ser	Leu	Gln	Glu	Tyr	Leu	Gln	Asn		
305					310					315					320		
Asp	Thr	Gly	Ser	Lys	Ile	His	Leu	Thr	Gln	Gln	Val	Asp	Met	Ala	Ala		
				325					330					335			
Gln	Val	Ala	Ser	Gly	Met	Ala	Tyr	Leu	Glu	Ser	Arg	Asn	Tyr	Ile	His		
			340					345					350				
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Val	Gly	Glu	His	Asn	Ile	Tyr		
	355						360					365					
Lys	Val	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Val	Phe	Lys	Val	Asp	Asn	Glu		
	370					375					380						
Asp	Ile	Tyr	Glu	Ser	Arg	His	Glu	Ile	Lys	Leu	Pro	Val	Lys	Trp	Thr		
385					390					395					400		
Ala	Pro	Glu	Ala	Ile	Arg	Ser	Asn	Lys	Phe	Ser	Ile	Lys	Ser	Asp	Val		
				405					410					415			
Trp	Ser	Phe	Gly	Ile	Leu	Leu	Tyr	Glu	Ile	Ile	Thr	Tyr	Gly	Lys	Met		
			420					425					430				
Pro	Tyr	Ser	Gly	Met	Thr	Gly	Ala	Gln	Val	Ile	Gln	Met	Leu	Ala	Gln		
	435						440					445					
Asn	Tyr	Arg	Leu	Pro	Gln	Pro	Ser	Asn	Cys	Pro	Gln	Gln	Phe	Tyr	Asn		
	450					455					460						
Ile	Met	Leu	Glu	Cys	Trp	Asn	Ala	Glu	Pro	Lys	Glu	Arg	Pro	Thr	Phe		
465					470					475					480		
Glu	Thr	Leu	Arg	Trp	Lys	Leu	Glu	Asp	Tyr	Phe	Glu	Thr	Asp	Ser	Ser		
				485					490					495			

Tyr Ser Asp Ala Asn Asn Phe Ile Arg
 500 505

<210> 7
 <211> 450
 <212> PRT
 <213> Homo sapiens

<400> 7
 Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr Glu Cys Ile Ala
 1 5 10 15
 Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu Pro Phe Cys Lys
 20 25 30
 Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp Pro Asn Trp Tyr
 35 40 45
 Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile Pro Ala Asn Tyr
 50 55 60
 Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys Leu Ser Leu Met
 65 70 75 80
 Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala Glu Arg Leu Leu
 85 90 95
 Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu Ser Thr Asn Tyr
 100 105 110
 Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly Lys Val Glu His
 115 120 125
 Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile Asp Glu Glu Val
 130 135 140
 Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr Thr Ser Asp Ala
 145 150 155 160
 Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val Met Glu Gly Thr
 165 170 175
 Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp Ala Leu Asn Met
 180 185 190
 Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly Glu Phe Gly Asp
 195 200 205
 Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala Val Lys Cys Ile
 210 215 220
 Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser Val Met
 225 230 235 240
 Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val Ile Val
 245 250 255

Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly
260 265 270

Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu Gly Gly
275 280 285

Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr
290 295 300

Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val
305 310 315 320

Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr
325 330 335

Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val Lys Trp
340 345 350

Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys Ser Asp
355 360 365

Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr Ser Phe Gly Arg
370 375 380

Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg Val Glu
385 390 395 400

Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala Val Tyr
405 410 415

Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg Pro Ser
420 425 430

Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His Glu Leu
435 440 445

His Leu
450

<210> 8

<211> 659

<212> PRT

<213> Homo sapiens

<400> 8

Met Ala Ala Val Ile Leu Glu Ser Ile Phe Leu Lys Arg Ser Gln Gln
1 5 10 15

Lys Lys Lys Thr Ser Pro Leu Asn Phe Lys Lys Arg Leu Phe Leu Leu
20 25 30

Thr Val His Lys Leu Ser Tyr Tyr Glu Tyr Asp Phe Glu Arg Gly Arg
35 40 45

Arg Gly Ser Lys Lys Gly Ser Ile Asp Val Glu Lys Ile Thr Cys Val
50 55 60

Glu	Thr	Val	Val	Pro	Glu	Lys	Asn	Pro	Pro	Pro	Glu	Arg	Gln	Ile	Pro	65	70	75	80
Arg	Arg	Gly	Glu	Glu	Ser	Ser	Glu	Met	Glu	Gln	Ile	Ser	Ile	Ile	Glu	85	90	95	
Arg	Phe	Pro	Tyr	Pro	Phe	Gln	Val	Val	Tyr	Asp	Glu	Gly	Pro	Leu	Tyr	100	105	110	
Val	Phe	Ser	Pro	Thr	Glu	Glu	Leu	Arg	Lys	Arg	Trp	Ile	His	Gln	Leu	115	120	125	
Lys	Asn	Val	Ile	Arg	Tyr	Asn	Ser	Asp	Leu	Val	Gln	Lys	Tyr	His	Pro	130	135	140	
Cys	Phe	Trp	Ile	Asp	Gly	Gln	Tyr	Leu	Cys	Cys	Ser	Gln	Thr	Ala	Lys	145	150	155	160
Asn	Ala	Met	Gly	Cys	Gln	Ile	Leu	Glu	Asn	Arg	Asn	Gly	Ser	Leu	Lys	165	170	175	
Pro	Gly	Ser	Ser	His	Arg	Lys	Thr	Lys	Lys	Pro	Leu	Pro	Pro	Thr	Pro	180	185	190	
Glu	Glu	Asp	Gln	Ile	Leu	Lys	Lys	Pro	Leu	Pro	Pro	Glu	Pro	Ala	Ala	195	200	205	
Ala	Pro	Val	Ser	Thr	Ser	Glu	Leu	Lys	Lys	Val	Val	Ala	Leu	Tyr	Asp	210	215	220	
Tyr	Met	Pro	Met	Asn	Ala	Asn	Asp	Leu	Gln	Leu	Arg	Lys	Gly	Asp	Glu	225	230	235	240
Tyr	Phe	Ile	Leu	Glu	Glu	Ser	Asn	Leu	Pro	Trp	Trp	Arg	Ala	Arg	Asp	245	250	255	
Lys	Asn	Gly	Gln	Glu	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Thr	Glu	Ala	260	265	270	
Glu	Asp	Ser	Ile	Glu	Met	Tyr	Glu	Trp	Tyr	Ser	Lys	His	Met	Thr	Arg	275	280	285	
Ser	Gln	Ala	Glu	Gln	Leu	Leu	Lys	Gln	Glu	Gly	Lys	Glu	Gly	Gly	Phe	290	295	300	
Ile	Val	Arg	Asp	Ser	Ser	Lys	Ala	Gly	Lys	Tyr	Thr	Val	Ser	Val	Phe	305	310	315	320
Ala	Lys	Ser	Thr	Gly	Asp	Pro	Gln	Gly	Val	Ile	Arg	His	Tyr	Val	Val	325	330	335	
Cys	Ser	Thr	Pro	Gln	Ser	Gln	Tyr	Tyr	Leu	Ala	Glu	Lys	His	Leu	Phe	340	345	350	
Ser	Thr	Ile	Pro	Glu	Leu	Ile	Asn	Tyr	His	Gln	His	Asn	Ser	Ala	Gly	355	360	365	

Leu Ile Ser Arg Leu Lys Tyr Pro Val Ser Gln Gln Asn Lys Asn Ala
 370 375 380
 Pro Ser Thr Ala Gly Leu Gly Tyr Gly Ser Trp Glu Ile Asp Pro Lys
 385 390 395 400
 Asp Leu Thr Phe Leu Lys Glu Leu Gly Thr Gly Gln Phe Gly Val Val
 405 410 415
 Lys Tyr Gly Lys Trp Arg Gly Gln Tyr Asp Val Ala Ile Lys Met Ile
 420 425 430
 Lys Glu Gly Ser Met Ser Glu Asp Glu Phe Ile Glu Glu Ala Lys Val
 435 440 445
 Met Met Asn Leu Ser His Glu Lys Leu Val Gln Leu Tyr Gly Val Cys
 450 455 460
 Thr Lys Gln Arg Pro Ile Phe Ile Ile Thr Glu Tyr Met Ala Asn Gly
 465 470 475 480
 Cys Leu Leu Asn Tyr Leu Arg Glu Met Arg His Arg Phe Gln Thr Gln
 485 490 495
 Gln Leu Leu Glu Met Cys Lys Asp Val Cys Glu Ala Met Glu Tyr Leu
 500 505 510
 Glu Ser Lys Gln Phe Leu His Arg Asp Leu Ala Ala Arg Asn Cys Leu
 515 520 525
 Val Asn Asp Gln Gly Val Val Lys Val Ser Asp Phe Gly Leu Ser Arg
 530 535 540
 Tyr Val Leu Asp Asp Glu Tyr Thr Ser Ser Val Gly Ser Lys Phe Pro
 545 550 555 560
 Val Arg Trp Ser Pro Pro Glu Val Leu Met Tyr Ser Lys Phe Ser Ser
 565 570 575
 Lys Ser Asp Ile Trp Ala Phe Gly Val Leu Met Trp Glu Ile Tyr Ser
 580 585 590
 Leu Gly Lys Met Pro Tyr Glu Arg Phe Thr Asn Ser Glu Thr Ala Glu
 595 600 605
 His Ile Ala Gln Gly Leu Arg Leu Tyr Arg Pro His Leu Ala Ser Glu
 610 615 620
 Lys Val Tyr Thr Ile Met Tyr Ser Cys Trp His Glu Lys Ala Asp Glu
 625 630 635 640
 Arg Pro Thr Phe Lys Ile Leu Leu Ser Asn Ile Leu Asp Val Met Asp
 645 650 655
 Glu Glu Ser

<210> 9

<211> 620

<212> PRT

<213> Homo sapiens

<400> 9

Met	Asn	Asn	Phe	Ile	Leu	Leu	Glu	Glu	Gln	Leu	Ile	Lys	Lys	Ser	Gln
1				5					10					15	

Gln	Lys	Arg	Arg	Thr	Ser	Pro	Ser	Asn	Phe	Lys	Val	Arg	Phe	Phe	Val
			20					25					30		

Leu	Thr	Lys	Ala	Ser	Leu	Ala	Tyr	Phe	Glu	Asp	Arg	His	Gly	Lys	Lys
		35					40					45			

Arg	Thr	Leu	Lys	Gly	Ser	Ile	Glu	Leu	Ser	Arg	Ile	Lys	Cys	Val	Glu
	50					55					60				

Ile	Val	Lys	Ser	Asp	Ile	Ser	Ile	Pro	Cys	His	Tyr	Lys	Tyr	Pro	Phe
65					70					75					80

Gln	Val	Val	His	Asp	Asn	Tyr	Leu	Leu	Tyr	Val	Phe	Ala	Pro	Asp	Arg
				85					90					95	

Glu	Ser	Arg	Gln	Arg	Trp	Val	Leu	Ala	Leu	Lys	Glu	Glu	Thr	Arg	Asn
			100					105						110	

Asn	Asn	Ser	Leu	Val	Pro	Lys	Tyr	His	Pro	Asn	Phe	Trp	Met	Asp	Gly
		115					120					125			

Lys	Trp	Arg	Cys	Cys	Ser	Gln	Leu	Glu	Lys	Leu	Ala	Thr	Gly	Cys	Ala
	130					135					140				

Gln	Tyr	Asp	Pro	Thr	Lys	Asn	Ala	Ser	Lys	Lys	Pro	Leu	Pro	Pro	Thr
145					150					155					160

Pro	Glu	Asp	Asn	Arg	Arg	Pro	Leu	Trp	Glu	Pro	Glu	Glu	Thr	Val	Val
			165						170					175	

Ile	Ala	Leu	Tyr	Asp	Tyr	Gln	Thr	Asn	Asp	Pro	Gln	Glu	Leu	Ala	Leu
		180						185					190		

Arg	Arg	Asn	Glu	Glu	Tyr	Cys	Leu	Leu	Asp	Ser	Ser	Glu	Ile	His	Trp
		195					200					205			

Trp	Arg	Val	Gln	Asp	Arg	Asn	Gly	His	Glu	Gly	Tyr	Val	Pro	Ser	Ser
	210					215					220				

Tyr	Leu	Val	Glu	Lys	Ser	Pro	Asn	Asn	Leu	Glu	Thr	Tyr	Glu	Trp	Tyr
225					230					235					240

Asn	Lys	Ser	Ile	Ser	Arg	Asp	Lys	Ala	Glu	Lys	Leu	Leu	Leu	Asp	Thr
			245						250					255	

Gly	Lys	Glu	Gly	Ala	Phe	Met	Val	Arg	Asp	Ser	Arg	Thr	Ala	Gly	Thr
			260					265					270		

Tyr	Thr	Val	Ser	Val	Phe	Thr	Lys	Ala	Val	Val	Ser	Glu	Asn	Asn	Pro	275	280	285
Cys	Ile	Lys	His	Tyr	His	Ile	Lys	Glu	Thr	Asn	Asp	Asn	Pro	Lys	Arg	290	295	300
Tyr	Tyr	Val	Ala	Glu	Lys	Tyr	Val	Phe	Asp	Ser	Ile	Pro	Leu	Leu	Ile	305	310	315
Asn	Tyr	His	Gln	His	Asn	Gly	Gly	Gly	Leu	Val	Thr	Arg	Leu	Arg	Tyr	325	330	335
Pro	Val	Cys	Phe	Gly	Arg	Gln	Lys	Ala	Pro	Val	Thr	Ala	Gly	Leu	Arg	340	345	350
Tyr	Gly	Lys	Trp	Val	Ile	Asp	Pro	Ser	Glu	Leu	Thr	Phe	Val	Gln	Glu	355	360	365
Ile	Gly	Ser	Gly	Gln	Phe	Gly	Leu	Val	His	Leu	Gly	Tyr	Trp	Leu	Asn	370	375	380
Lys	Asp	Lys	Val	Ala	Ile	Lys	Thr	Ile	Arg	Glu	Gly	Ala	Met	Ser	Glu	385	390	395
Glu	Asp	Phe	Ile	Glu	Glu	Ala	Glu	Val	Met	Met	Lys	Leu	Ser	His	Pro	405	410	415
Lys	Leu	Val	Gln	Leu	Tyr	Gly	Val	Cys	Leu	Glu	Gln	Ala	Pro	Ile	Cys	420	425	430
Leu	Val	Phe	Glu	Phe	Met	Glu	His	Gly	Cys	Leu	Ser	Asp	Tyr	Leu	Arg	435	440	445
Thr	Gln	Arg	Gly	Leu	Phe	Ala	Ala	Glu	Thr	Leu	Leu	Gly	Met	Cys	Leu	450	455	460
Asp	Val	Cys	Glu	Gly	Met	Ala	Tyr	Leu	Glu	Glu	Ala	Cys	Val	Ile	His	465	470	475
Arg	Asp	Leu	Ala	Ala	Arg	Asn	Cys	Leu	Val	Gly	Glu	Asn	Gln	Val	Ile	485	490	495
Lys	Val	Ser	Asp	Phe	Gly	Met	Thr	Arg	Phe	Val	Leu	Asp	Asp	Gln	Tyr	500	505	510
Thr	Ser	Ser	Thr	Gly	Thr	Lys	Phe	Pro	Val	Lys	Trp	Ala	Ser	Pro	Glu	515	520	525
Val	Phe	Ser	Phe	Ser	Arg	Tyr	Ser	Ser	Lys	Ser	Asp	Val	Trp	Ser	Phe	530	535	540
Gly	Val	Leu	Met	Trp	Glu	Val	Phe	Ser	Glu	Gly	Lys	Ile	Pro	Tyr	Glu	545	550	555
Asn	Arg	Ser	Asn	Ser	Glu	Val	Val	Glu	Asp	Ile	Ser	Thr	Gly	Phe	Arg	565	570	575

Leu Tyr Lys Pro Arg Leu Ala Ser Thr His Val Tyr Gln Ile Met Asn
 580 585 590

His Cys Trp Lys Glu Arg Pro Glu Asp Arg Pro Ala Phe Ser Arg Leu
 595 600 605

Leu Arg Gln Leu Ala Glu Ile Ala Glu Ser Gly Leu
 610 615 620

<210> 10

<211> 527

<212> PRT

<213> Mus sp.

<400> 10

Met Met Val Ser Phe Pro Val Lys Ile Asn Phe His Ser Ser Pro Gln
 1 5 10 15

Ser Arg Asp Arg Trp Val Lys Lys Leu Lys Glu Glu Ile Lys Asn Asn
 20 25 30

Asn Asn Ile Met Ile Lys Tyr His Pro Lys Phe Trp Ala Asp Gly Ser
 35 40 45

Tyr Gln Cys Cys Arg Gln Thr Glu Lys Leu Ala Pro Gly Cys Glu Lys
 50 55 60

Tyr Asn Leu Phe Glu Ser Ser Ile Arg Lys Thr Leu Pro Pro Ala Pro
 65 70 75 80

Glu Ile Lys Lys Arg Arg Pro Pro Pro Pro Ile Pro Pro Glu Glu Glu
 85 90 95

Asn Thr Glu Glu Ile Val Val Ala Met Tyr Asp Phe Gln Ala Thr Glu
 100 105 110

Ala His Asp Leu Arg Leu Glu Arg Gly Gln Glu Tyr Ile Ile Leu Glu
 115 120 125

Lys Asn Asp Leu His Trp Trp Arg Ala Arg Asp Lys Tyr Gly Trp Tyr
 130 135 140

Cys Arg Asn Thr Asn Arg Ser Lys Ala Glu Gln Leu Leu Arg Thr Glu
 145 150 155 160

Asp Lys Glu Gly Gly Phe Met Val Arg Asp Ser Ser Gln Pro Gly Leu
 165 170 175

Tyr Thr Val Ser Leu Tyr Thr Lys Phe Gly Gly Glu Gly Ser Ser Gly
 180 185 190

Phe Arg His Tyr His Ile Lys Glu Thr Ala Thr Ser Pro Lys Lys Tyr
 195 200 205

Tyr Leu Ala Glu Lys His Ala Phe Gly Ser Ile Pro Glu Ile Ile Glu
 210 215 220

Tyr	His	Lys	His	Asn	Ala	Ala	Gly	Leu	Val	Thr	Arg	Leu	Arg	Tyr	Pro	225	230	235	240
Val	Ser	Thr	Lys	Gly	Lys	Asn	Ala	Pro	Thr	Thr	Ala	Gly	Phe	Ser	Tyr	245	250	255	
Asp	Lys	Trp	Glu	Ile	Asn	Pro	Ser	Glu	Leu	Thr	Phe	Met	Arg	Glu	Leu	260	265	270	
Gly	Ser	Gly	Leu	Phe	Gly	Val	Val	Arg	Leu	Gly	Lys	Trp	Arg	Ala	Gln	275	280	285	
Tyr	Lys	Val	Ala	Ile	Lys	Ala	Ile	Arg	Glu	Gly	Ala	Met	Cys	Glu	Glu	290	295	300	
Asp	Phe	Ile	Glu	Glu	Ala	Lys	Val	Met	Met	Lys	Leu	Thr	His	Pro	Lys	305	310	315	320
Leu	Val	Gln	Leu	Tyr	Gly	Val	Cys	Thr	Gln	Gln	Lys	Pro	Ile	Tyr	Ile	325	330	335	
Val	Thr	Glu	Phe	Met	Glu	Arg	Gly	Cys	Leu	Leu	Asn	Phe	Leu	Arg	Gln	340	345	350	
Arg	Gln	Gly	His	Phe	Ser	Arg	Asp	Met	Leu	Leu	Ser	Met	Cys	Gln	Asp	355	360	365	
Val	Cys	Glu	Gly	Met	Glu	Tyr	Leu	Glu	Arg	Asn	Ser	Phe	Ile	His	Arg	370	375	380	
Asp	Leu	Ala	Ala	Arg	Asn	Cys	Leu	Val	Asn	Glu	Ala	Gly	Val	Val	Lys	385	390	395	400
Val	Ser	Asp	Phe	Gly	Met	Ala	Arg	Tyr	Val	Leu	Asp	Asp	Gln	Tyr	Thr	405	410	415	
Ser	Ser	Ser	Gly	Ala	Lys	Phe	Pro	Val	Lys	Trp	Cys	Pro	Pro	Glu	Val	420	425	430	
Phe	Asn	Tyr	Ser	Arg	Phe	Ser	Ser	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	435	440	445	
Val	Leu	Met	Trp	Glu	Ile	Phe	Thr	Glu	Gly	Arg	Met	Pro	Phe	Glu	Lys	450	455	460	
Asn	Thr	Asn	Tyr	Glu	Val	Val	Thr	Met	Val	Thr	Arg	Gly	His	Arg	Leu	465	470	475	480
His	Arg	Pro	Lys	Leu	Ala	Thr	Lys	Tyr	Leu	Tyr	Glu	Val	Met	Leu	Arg	485	490	495	
Cys	Trp	Gln	Glu	Arg	Pro	Glu	Gly	Arg	Pro	Ser	Phe	Glu	Asp	Leu	Leu	500	505	510	
Arg	Thr	Ile	Asp	Glu	Leu	Val	Glu	Cys	Glu	Glu	Thr	Phe	Gly	Arg		515	520	525	

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu
1 5 10 15

Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr
20 25 30

Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro
35 40 45

Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe
50 55 60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly
65 70 75 80

Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg
85 90 95

Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu
100 105 110

Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly
115 120 125

Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile
130 135 140

Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu
145 150 155 160

Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg
165 170 175

Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp
180 185 190

Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu
195 200 205

Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu
210 215 220

Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys
225 230 235 240

Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu
245 250 255

Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln
260 265 270

Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly
 275 280 285
 Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly
 290 295 300
 Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys
 305 310 315 320
 Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu
 325 330 335
 Pro Ile Tyr Ile Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp
 340 345 350
 Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val
 355 360 365
 Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met
 370 375 380
 Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn
 385 390 395 400
 Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu
 405 410 415
 Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp
 420 425 430
 Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp
 435 440 445
 Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg
 450 455 460
 Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu
 465 470 475 480
 Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His
 485 490 495
 Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr
 500 505 510
 Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu
 515 520 525
 Pro Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535

<210> 12

<211> 536

<212> PRT

<213> Gallus gallus

<400> 12

Met	Gly	Cys	Val	His	Cys	Lys	Glu	Lys	Ile	Ser	Gly	Lys	Gly	Gln	Gly	1	5	10	15
Gly	Ser	Gly	Thr	Gly	Thr	Pro	Ala	His	Pro	Pro	Ser	Gln	Tyr	Asp	Pro	20	25	30	
Asp	Pro	Thr	Gln	Leu	Ser	Gly	Ala	Phe	Thr	His	Ile	Pro	Asp	Phe	Asn	35	40	45	
Asn	Phe	His	Ala	Ala	Ala	Val	Ser	Pro	Pro	Val	Pro	Phe	Ser	Gly	Pro	50	55	60	
Gly	Phe	Tyr	Pro	Cys	Asn	Thr	Leu	Gln	Ala	His	Ser	Ser	Ile	Thr	Gly	65	70	75	80
Gly	Gly	Val	Thr	Leu	Phe	Ile	Ala	Leu	Tyr	Asp	Tyr	Glu	Ala	Arg	Thr	85	90	95	
Glu	Asp	Asp	Leu	Ser	Phe	Gln	Lys	Gly	Glu	Lys	Phe	His	Ile	Ile	Asn	100	105	110	
Asn	Thr	Glu	Gly	Asp	Trp	Trp	Glu	Ala	Arg	Ser	Leu	Ser	Ser	Gly	Ala	115	120	125	
Thr	Gly	Tyr	Ile	Pro	Ser	Asn	Tyr	Val	Ala	Pro	Val	Asp	Ser	Ile	Gln	130	135	140	
Ala	Glu	Glu	Trp	Tyr	Phe	Gly	Lys	Ile	Gly	Arg	Lys	Asp	Ala	Glu	Arg	145	150	155	160
Gln	Leu	Leu	Cys	His	Gly	Asn	Cys	Arg	Gly	Thr	Phe	Leu	Ile	Arg	Glu	165	170	175	
Ser	Glu	Thr	Thr	Lys	Gly	Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp	Asp	180	185	190	
Glu	Ala	Lys	Gly	Asp	His	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp	195	200	205	
Ser	Gly	Gly	Tyr	Tyr	Ile	Thr	Thr	Arg	Ala	Gln	Phe	Asp	Thr	Ile	Gln	210	215	220	
Gln	Leu	Val	Gln	His	Tyr	Ile	Glu	Arg	Ala	Ala	Gly	Leu	Cys	Cys	Arg	225	230	235	240
Leu	Ala	Val	Pro	Cys	Pro	Lys	Gly	Thr	Pro	Lys	Leu	Ala	Asp	Leu	Ser	245	250	255	
Val	Lys	Thr	Lys	Asp	Val	Trp	Glu	Ile	Pro	Arg	Glu	Ser	Leu	Gln	Leu	260	265	270	
Leu	Gln	Lys	Leu	Gly	Asn	Gly	Gln	Phe	Gly	Glu	Val	Trp	Met	Gly	Thr	275	280	285	
Trp	Asn	Gly	Thr	Thr	Lys	Val	Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr	290	295	300	

Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu
 305 310 315 320
 Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
 325 330 335
 Ile Tyr Ile Val Thr Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe
 340 345 350
 Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp
 355 360 365
 Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn
 370 375 380
 Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn
 385 390 395 400
 Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
 405 410 415
 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
 420 425 430
 Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val
 435 440 445
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val
 450 455 460
 Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg
 465 470 475 480
 Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp
 485 490 495
 Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe
 500 505 510
 Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro
 515 520 525
 Gln Tyr Gln Pro Gly Asp Asn Gln
 530 535

<210> 13

<211> 536

<212> PRT

<213> Homo sapiens

<400> 13

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
 1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe
 20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
 35 40 45
 Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
 50 55 60
 Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
 65 70 75 80
 Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
 85 90 95
 Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
 100 105 110
 Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
 115 120 125
 Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
 130 135 140
 Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
 145 150 155 160
 Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
 165 170 175
 Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
 180 185 190
 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
 195 200 205
 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
 210 215 220
 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
 225 230 235 240
 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
 245 250 255
 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
 260 265 270
 Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr
 275 280 285
 Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr
 290 295 300
 Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu
 305 310 315 320
 Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
 325 330 335

Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe
 340 345 350
 Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp
 355 360 365
 Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn
 370 375 380
 Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
 385 390 395 400
 Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
 405 410 415
 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
 420 425 430
 Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
 435 440 445
 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val
 450 455 460
 Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg
 465 470 475 480
 Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
 485 490 495
 Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
 500 505 510
 Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
 515 520 525
 Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535

<210> 14
 <211> 543
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr
 1 5 10 15
 Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr
 20 25 30
 Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys
 35 40 45
 Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly
 50 55 60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val
 65 70 75 80
 Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe
 85 90 95
 Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe
 100 105 110
 Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp
 115 120 125
 Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser
 130 135 140
 Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe
 145 150 155 160
 Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly
 165 170 175
 Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly
 180 185 190
 Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn
 195 200 205
 Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile
 210 215 220
 Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr
 225 230 235 240
 Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro
 245 250 255
 Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile
 260 265 270
 Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe
 275 280 285
 Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile
 290 295 300
 Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu
 305 310 315 320
 Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr
 325 330 335
 Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser
 340 345 350
 Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu
 355 360 365

Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met
 370 375 380
 Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 385 390 395 400
 Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly
 405 410 415
 Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala
 420 425 430
 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg
 435 440 445
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu
 450 455 460
 Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu
 465 470 475 480
 Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
 485 490 495
 Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp
 500 505 510
 Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp
 515 520 525
 Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535 540

<210> 15
 <211> 529
 <212> PRT
 <213> Homo sapiens

<400> 15
 Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys
 1 5 10 15
 Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp
 20 25 30
 His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala
 35 40 45
 His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly
 50 55 60
 Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr
 65 70 75 80
 Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu
 85 90 95

Thr	Phe	Thr	Lys	Gly	Glu	Lys	Phe	His	Ile	Leu	Asn	Asn	Thr	Glu	Gly	100	105	110	
Asp	Trp	Trp	Glu	Ala	Arg	Ser	Leu	Ser	Ser	Gly	Lys	Thr	Gly	Cys	Ile	115	120	125	
Pro	Ser	Asn	Tyr	Val	Ala	Pro	Val	Asp	Ser	Ile	Gln	Ala	Glu	Glu	Trp	130	135	140	
Tyr	Phe	Gly	Lys	Ile	Gly	Arg	Lys	Asp	Ala	Glu	Arg	Gln	Leu	Leu	Ser	145	150	155	160
Pro	Gly	Asn	Pro	Gln	Gly	Ala	Phe	Leu	Ile	Arg	Glu	Ser	Glu	Thr	Thr	165	170	175	
Lys	Gly	Ala	Tyr	Ser	Leu	Ser	Ile	Arg	Asp	Trp	Asp	Gln	Thr	Arg	Gly	180	185	190	
Asp	His	Val	Lys	His	Tyr	Lys	Ile	Arg	Lys	Leu	Asp	Met	Gly	Gly	Tyr	195	200	205	
Tyr	Ile	Thr	Thr	Arg	Val	Gln	Phe	Asn	Ser	Val	Gln	Glu	Leu	Val	Gln	210	215	220	
His	Tyr	Met	Glu	Val	Asn	Asp	Gly	Leu	Cys	Asn	Leu	Leu	Ile	Ala	Pro	225	230	235	240
Cys	Thr	Ile	Met	Lys	Pro	Gln	Thr	Leu	Gly	Leu	Ala	Lys	Asp	Ala	Trp	245	250	255	
Glu	Ile	Ser	Arg	Ser	Ser	Ile	Thr	Leu	Glu	Arg	Arg	Leu	Gly	Thr	Gly	260	265	270	
Cys	Phe	Gly	Asp	Val	Trp	Leu	Gly	Thr	Trp	Asn	Gly	Ser	Thr	Lys	Val	275	280	285	
Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Ser	Pro	Lys	Ala	Phe	Leu	290	295	300	
Glu	Glu	Ala	Gln	Val	Met	Lys	Leu	Leu	Arg	His	Asp	Lys	Leu	Val	Gln	305	310	315	320
Leu	Tyr	Ala	Val	Val	Ser	Glu	Glu	Pro	Ile	Tyr	Ile	Val	Thr	Glu	Phe	325	330	335	
Met	Cys	His	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Asn	Pro	Glu	Gly	Gln	340	345	350	
Asp	Leu	Arg	Leu	Pro	Gln	Leu	Val	Asp	Met	Ala	Ala	Gln	Val	Ala	Glu	355	360	365	
Gly	Met	Ala	Tyr	Met	Glu	Arg	Met	Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg	370	375	380	
Ala	Ala	Asn	Ile	Leu	Val	Gly	Glu	Arg	Leu	Ala	Cys	Lys	Ile	Ala	Asp	385	390	395	400

Phe	Gly	Leu	Ala	Arg	Leu	Ile	Lys	Asp	Asp	Glu	Tyr	Asn	Pro	Cys	Gln		
				405					410					415			
Gly	Ser	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ala	Leu	Phe		
				420					425					430			
Gly	Arg	Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu	Leu		
				435					440					445			
Thr	Glu	Leu	Ile	Thr	Lys	Gly	Arg	Ile	Pro	Tyr	Pro	Gly	Met	Asn	Lys		
				450					455					460			
Arg	Glu	Val	Leu	Glu	Gln	Val	Glu	Gln	Gly	Tyr	His	Met	Pro	Cys	Pro		
465					470					475					480		
Pro	Gly	Cys	Pro	Ala	Ser	Leu	Tyr	Glu	Ala	Met	Glu	Gln	Thr	Trp	Arg		
				485					490					495			
Leu	Asp	Pro	Glu	Glu	Arg	Pro	Thr	Phe	Glu	Tyr	Leu	Gln	Ser	Phe	Leu		
				500					505					510			
Glu	Asp	Tyr	Phe	Thr	Ser	Ala	Glu	Pro	Gln	Tyr	Gln	Pro	Gly	Asp	Gln		
				515					520					525			

Thr

```
<210> 16
<211> 512
<212> PRT
<213> Homo sapiens
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<400> 16
Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly
  1          5          10          15
Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr
          20          25          30
Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser
          35          40          45
Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln
          50          55          60
Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp
  65          70          75          80
Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His
          85          90          95
Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe
          100          105          110
Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu
          115          120          125

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Trp	Phe	Phe	Lys	Asp	Ile	Thr	Arg	Lys	Asp	Ala	Glu	Arg	Gln	Leu	Leu		
130						135						140					
Ala	Pro	Gly	Asn	Ser	Ala	Gly	Ala	Phe	Leu	Ile	Arg	Glu	Ser	Glu	Thr		
145						150						155					
Leu	Lys	Gly	Ser	Phe	Ser	Leu	Ser	Val	Arg	Asp	Phe	Asp	Pro	Val	His		
				165						170							
Gly	Asp	Val	Ile	Lys	His	Tyr	Lys	Ile	Arg	Ser	Leu	Asp	Asn	Gly	Gly		
			180						185						190		
Tyr	Tyr	Ile	Ser	Pro	Arg	Ile	Thr	Phe	Pro	Cys	Ile	Ser	Asp	Met	Ile		
		195						200						205			
Lys	His	Tyr	Gln	Lys	Gln	Ala	Asp	Gly	Leu	Cys	Arg	Arg	Leu	Glu	Lys		
210						215						220					
Ala	Cys	Ile	Ser	Pro	Lys	Pro	Gln	Lys	Pro	Trp	Asp	Lys	Asp	Ala	Trp		
225						230						235		240			
Glu	Ile	Pro	Arg	Glu	Ser	Ile	Lys	Leu	Val	Lys	Arg	Leu	Gly	Ala	Gly		
				245						250						255	
Gln	Phe	Gly	Glu	Val	Trp	Met	Gly	Tyr	Tyr	Asn	Asn	Ser	Thr	Lys	Val		
			260						265						270		
Ala	Val	Lys	Thr	Leu	Lys	Pro	Gly	Thr	Met	Ser	Val	Gln	Ala	Phe	Leu		
		275						280						285			
Glu	Glu	Ala	Asn	Leu	Met	Lys	Thr	Leu	Gln	His	Asp	Lys	Leu	Val	Arg		
290						295						300					
Leu	Tyr	Ala	Val	Val	Thr	Arg	Glu	Glu	Pro	Ile	Tyr	Ile	Ile	Thr	Glu		
				310						315						320	
Tyr	Met	Ala	Lys	Gly	Ser	Leu	Leu	Asp	Phe	Leu	Lys	Ser	Asp	Glu	Gly		
				325						330						335	
Gly	Lys	Val	Leu	Leu	Pro	Lys	Leu	Ile	Asp	Phe	Ser	Ala	Gln	Ile	Ala		
			340						345						350		
Glu	Gly	Met	Ala	Tyr	Ile	Glu	Arg	Lys	Asn	Tyr	Ile	His	Arg	Asp	Leu		
		355						360						365			
Arg	Ala	Ala	Asn	Val	Leu	Val	Ser	Glu	Ser	Leu	Met	Cys	Lys	Ile	Ala		
370						375						380					
Asp	Phe	Gly	Leu	Ala	Arg	Val	Ile	Glu	Asp	Asn	Glu	Tyr	Thr	Ala	Arg		
385						390						395		400			
Glu	Gly	Ala	Lys	Phe	Pro	Ile	Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Asn		
				405						410						415	
Phe	Gly	Cys	Phe	Thr	Ile	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu		
			420						425						430		

Leu Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr
 435 440 445
 Asn Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg
 450 455 460
 Val Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp
 465 470 475 480
 Lys Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val
 485 490 495
 Leu Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Gln Pro
 500 505 510

<210> 17
 <211> 505
 <212> PRT
 <213> Homo sapiens

<400> 17
 Met Gly Ser Met Lys Ser Lys Phe Leu Gln Val Gly Gly Asn Thr Phe
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 Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro Val Tyr Val Pro
 20 25 30
 Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser His Asn Ser Asn
 35 40 45
 Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile Ile Val Val Ala
 50 55 60
 Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe Gln Lys
 65 70 75 80
 Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu Trp Trp Lys Ala
 85 90 95
 Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val
 100 105 110
 Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe Phe Lys Gly Ile
 115 120 125
 Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro Gly Asn Met Leu
 130 135 140
 Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys Gly Ser Tyr Ser
 145 150 155 160
 Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp Thr Val Lys His
 165 170 175
 Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr Ile Ser Pro Arg
 180 185 190

Ser	Thr	Phe	Ser	Thr	Leu	Gln	Glu	Leu	Val	Asp	His	Tyr	Lys	Lys	Gly	195	200	205
Asn	Asp	Gly	Leu	Cys	Gln	Lys	Leu	Ser	Val	Pro	Cys	Met	Ser	Ser	Lys	210	215	220
Pro	Gln	Lys	Pro	Trp	Glu	Lys	Asp	Ala	Trp	Glu	Ile	Pro	Arg	Glu	Ser	225	230	235
Leu	Lys	Leu	Glu	Lys	Lys	Leu	Gly	Ala	Gly	Gln	Phe	Gly	Glu	Val	Trp	245	250	255
Met	Ala	Thr	Tyr	Asn	Lys	His	Thr	Lys	Val	Ala	Val	Lys	Thr	Met	Lys	260	265	270
Pro	Gly	Ser	Met	Ser	Val	Glu	Ala	Phe	Leu	Ala	Glu	Ala	Asn	Val	Met	275	280	285
Lys	Thr	Leu	Gln	His	Asp	Lys	Leu	Val	Lys	Leu	His	Ala	Val	Val	Thr	290	295	300
Lys	Glu	Pro	Ile	Tyr	Ile	Ile	Thr	Glu	Phe	Met	Ala	Lys	Gly	Ser	Leu	305	310	315
Leu	Asp	Phe	Leu	Lys	Ser	Asp	Glu	Gly	Ser	Lys	Gln	Pro	Leu	Pro	Lys	325	330	335
Leu	Ile	Asp	Phe	Ser	Ala	Gln	Ile	Ala	Glu	Gly	Met	Ala	Phe	Ile	Glu	340	345	350
Gln	Arg	Asn	Tyr	Ile	His	Arg	Asp	Leu	Arg	Ala	Ala	Asn	Ile	Leu	Val	355	360	365
Ser	Ala	Ser	Leu	Val	Cys	Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Val	370	375	380
Ile	Glu	Asp	Asn	Glu	Tyr	Thr	Ala	Arg	Glu	Gly	Ala	Lys	Phe	Pro	Ile	385	390	395
Lys	Trp	Thr	Ala	Pro	Glu	Ala	Ile	Asn	Phe	Gly	Ser	Phe	Thr	Ile	Lys	405	410	415
Ser	Asp	Val	Trp	Ser	Phe	Gly	Ile	Leu	Leu	Met	Glu	Ile	Val	Thr	Tyr	420	425	430
Gly	Arg	Ile	Pro	Tyr	Pro	Gly	Met	Ser	Asn	Pro	Glu	Val	Ile	Arg	Ala	435	440	445
Leu	Glu	Arg	Gly	Tyr	Arg	Met	Pro	Arg	Pro	Glu	Asn	Cys	Pro	Glu	Glu	450	455	460
Leu	Tyr	Asn	Ile	Met	Met	Arg	Cys	Trp	Lys	Asn	Arg	Pro	Glu	Glu	Arg	465	470	475
Pro	Thr	Phe	Glu	Tyr	Ile	Gln	Ser	Val	Leu	Asp	Asp	Phe	Tyr	Thr	Ala	485	490	495

Thr Glu Ser Gln Tyr Gln Gln Gln Pro
 500 505

<210> 18
 <211> 509
 <212> PRT
 <213> Homo sapiens

<400> 18
 Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn
 1 5 10 15
 Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly
 20 25 30
 Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu
 35 40 45
 Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn
 50 55 60
 Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu
 65 70 75 80
 Gly Phe Glu Lys Gly Glu Gln Leu Arg Ile Leu Glu Gln Ser Gly Glu
 85 90 95
 Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro
 100 105 110
 Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe
 115 120 125
 Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro
 130 135 140
 Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala
 145 150 155 160
 Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu
 165 170 175
 Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr
 180 185 190
 Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His
 195 200 205
 Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys
 210 215 220
 Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val
 225 230 235 240
 Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe
 245 250 255

Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val
 260 265 270
 Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu
 275 280 285
 Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr
 290 295 300
 Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Thr Glu Tyr Met Glu
 305 310 315 320
 Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu
 325 330 335
 Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met
 340 345 350
 Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 355 360 365
 Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly
 370 375 380
 Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala
 385 390 395 400
 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr
 405 410 415
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu
 420 425 430
 Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu
 435 440 445
 Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn
 450 455 460
 Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg
 465 470 475 480
 Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp
 485 490 495
 Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro
 500 505

<210> 19
 <211> 499
 <212> PRT
 <213> Mus sp.

<400> 19
 Met Gly Leu Leu Ser Ser Lys Arg Gln Val Ser Glu Lys Gly Lys Gly
 1 5 10 15

Trp Ser Pro Val Lys Ile Arg Thr Gln Asp Lys Ala Pro Pro Pro Leu
 20 25 30
 Pro Pro Leu Val Val Phe Asn His Leu Ala Pro Pro Ser Pro Asn Gln
 35 40 45
 Asp Pro Asp Glu Glu Glu Arg Phe Val Val Ala Leu Phe Asp Tyr Ala
 50 55 60
 Ala Val Asn Asp Arg Asp Leu Gln Val Leu Lys Gly Glu Lys Leu Gln
 65 70 75 80
 Val Leu Arg Ser Thr Gly Asp Trp Trp Leu Ala Arg Ser Leu Val Thr
 85 90 95
 Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe Val Ala Pro Val Glu Thr
 100 105 110
 Leu Glu Val Glu Lys Trp Phe Phe Arg Thr Ile Ser Arg Lys Asp Ala
 115 120 125
 Glu Arg Gln Leu Leu Ala Pro Met Asn Lys Ala Gly Ser Phe Leu Ile
 130 135 140
 Arg Glu Ser Glu Ser Asn Lys Gly Ala Phe Ser Leu Ser Val Lys Asp
 145 150 155 160
 Ile Thr Thr Gln Gly Glu Val Val Lys His Tyr Lys Ile Arg Ser Leu
 165 170 175
 Asp Asn Gly Gly Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Thr Leu
 180 185 190
 Gln Ala Leu Val Gln His Tyr Ser Lys Lys Gly Asp Gly Leu Cys Gln
 195 200 205
 Lys Leu Thr Leu Pro Cys Val Asn Leu Ala Pro Lys Asn Leu Trp Ala
 210 215 220
 Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser Leu Lys Leu Val Arg Lys
 225 230 235 240
 Leu Gly Ser Gly Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Lys Asn
 245 250 255
 Asn Met Lys Val Ala Ile Lys Thr Leu Lys Glu Gly Thr Met Ser Pro
 260 265 270
 Glu Ala Phe Leu Gly Glu Ala Asn Val Met Lys Thr Leu Gln His Glu
 275 280 285
 Arg Leu Val Arg Leu Tyr Ala Val Val Thr Arg Glu Pro Ile Tyr Ile
 290 295 300
 Val Thr Glu Tyr Met Ala Arg Gly Cys Leu Leu Asp Phe Leu Lys Thr
 305 310 315 320

Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg Leu Ile Asp Met Ser Ala
 325 330 335
 Gln Val Ala Glu Gly Met Ala Tyr Ile Glu Arg Met Asn Ser Ile His
 340 345 350
 Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Glu Thr Leu Cys Cys
 355 360 365
 Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile Ile Asp Ser Glu Tyr Thr
 370 375 380
 Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala
 385 390 395 400
 Ile His Phe Gly Val Phe Thr Ile Lys Ala Asp Val Trp Ser Phe Gly
 405 410 415
 Val Leu Leu Met Val Ile Val Thr Tyr Gly Arg Val Pro Tyr Pro Gly
 420 425 430
 Met Ser Asn Pro Glu Val Ile Arg Ser Leu Glu His Gly Tyr Arg Met
 435 440 445
 Pro Cys Pro Glu Thr Cys Pro Pro Glu Leu Tyr Asn Asp Ile Ile Thr
 450 455 460
 Glu Cys Trp Arg Gly Arg Pro Glu Glu Arg Pro Thr Phe Glu Phe Leu
 465 470 475 480
 Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Glu
 485 490 495
 Leu Gln Pro

<210> 20
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> modified_base
 <222> (14)
 <223> A, T, C, G, other or unknown

<220>
 <221> modified_base
 <222> (20)
 <223> A, T, C, G, other or unknown

<220>
 <221> modified_base
 <222> (23)
 <223> A, T, C, G, other or unknown

<220>
 <221> modified_base

<222> (26)
 <223> A, T, C, G, other or unknown
 <220>
 <223> Description of Artificial Sequence: Primer
 <400> 20
 ggaattccca ymgcnrayytn rcnrcnmng

28

<210> 21
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> modified_base
 <222> (12)
 <223> A, T, C, G, other or unknown

<220>
 <221> modified_base
 <222> (18)
 <223> A, T, C, G, other or unknown

<220>
 <221> modified_base
 <222> (24)
 <223> A, T, C, G, other or unknown

<220>
 <223> Description of Artificial Sequence: Primer
 <400> 21
 ggaattccrw rnswwcanac stcnsa

26

<210> 22
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 22
 Gly Gln Asp Ala Asp Gly Ser Thr Ser Pro Arg Ser Gln Glu Pro
 1 5 10 15

<210> 23
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 23

Gln Gln Leu Leu Ser Ser Ile Glu Pro Leu Arg Glu Lys Asp Lys His
1 5 10 15

<210> 24

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative peptide

<220>

<221> MOD_RES

<222> (6)

<223> Variable amino acid

<400> 24

Ser Asp Val Trp Ser Xaa
1 5

a14
cont